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**Anti-KIR light variable regions**

		1
DF-200 light variable	(1)	M--ESQT <del>L</del> VE <del>I</del> STILLW <del>I</del> YGA <del>D</del> G <del>N</del> IV <del>T</del> QSPKSMSM <del>S</del> GERV <del>T</del> ITCKASEN
PAN2D-Light-variable	(1)	MDFQVQ <del>I</del> IFSE <del>I</del> LLISAS <del>V</del> IM <del>S</del> RC <del>G</del> IV <del>T</del> QSPASMSA <del>S</del> GERV <del>T</del> ITCTASSS
Consensus	(1)	Q F I I L A GNIVITQSP SMS SLGERVLT <del>C</del> AS
	51	
DF-200 light variable	(49)	V <del>V</del> T-Y <del>V</del> SMYQQKBEQSP <del>K</del> LI <del>T</del> Y <del>G</del> ASNR <del>T</del> IGVPDR <del>F</del> IGSGSAT <del>D</del> E <del>T</del> LT <del>I</del> SS
PAN2D-Light-variable	(51)	V <del>S</del> SY <del>T</del> Y <del>V</del> WYQQKPGSSP <del>K</del> LI <del>T</del> Y <del>G</del> ASNR <del>T</del> IGVPDR <del>F</del> IGSGSAT <del>D</del> E <del>T</del> LT <del>I</del> SS
Consensus	(51)	V S Y <del>I</del> WYQQKP SPKL IY SN SGVP R <del>S</del> GSGSAT FSLT <del>I</del> SS
	101	
DF-200 light variable	(98)	W <del>Q</del> AED <del>L</del> AD <del>Y</del> CG <del>G</del> CSY <del>P</del> YTFGGGT <del>K</del> LE <del>I</del> KR (SEQ ID NO: 1)
PAN2D-Light-variable	(101)	W <del>Q</del> AED <del>A</del> AT <del>Y</del> CH <del>O</del> Y <del>R</del> RS <del>P</del> PT <del>F</del> GGGT <del>K</del> LE <del>I</del> KR (SEQ ID NO: 2)
Consensus	(101)	W AED A YHC Q H P T <del>F</del> GGGT <del>K</del> LE <del>I</del> KR (SEQ ID NO: 13)
	131	

Numbers above amino acid sequences indicate position respective to initiation of translation Met (+1) in the immature (non-secreted) immunoglobulin. Underlined are the CDR regions

**FIG 12**

<b>CDR's from the anti-KIR light variable regions</b>	
<b>CDR-L1 from clones PAN-2D and DF-200</b>	<b>CDR -L2 from clones PAN-2D and DF-200</b>
Residue before: Normally Cys. Residues after: Trp. Typically Trp-Tyr-Leu	Residues before: Generally Ile-Tyr
Length: 10-17 aa	Length: 7 aa
Start: approximately 24 aa from the beginning of secreted protein	Start: approximately 16 aa after the end of CDR-L1
DF-200 light variable (44) K <del>A</del> SEN <del>V</del> <del>V</del> <del>I</del> -Y <del>V</del> S (SEQ ID NO:3)	DF-200 light variable (70) G <del>A</del> SN <del>R</del> <del>M</del> (SEQ ID NO:5)
PAN2D-Light-variable (46) T <del>A</del> SS <del>S</del> <del>S</del> <del>S</del> Y (SEQ ID NO:4)	PAN2D-Light-variable (73) ST <del>S</del> N <del>L</del> <del>A</del> <del>S</del> (SEQ ID NO:6)
Consensus AS V S Y I (SEQ ID NO:14)	Consensus SN S (SEQ ID NO:15)
<b>CDR-L3 from clones PAN-2D and DF-200</b>	
Residues before: Cys	
Residues after: Phe-Gly-XXX-Gly	
Length: 7-11 aa	
Start: approximately 33 aa after the end of CDR-L2	
DF-200 light variable (109) G <del>Q</del> G <del>S</del> Y <del>P</del> Y (SEQ ID NO:7)	
PAN2D-Light-variable (112) H <del>Q</del> Y <del>R</del> RS <del>P</del> T (SEQ ID NO:8)	
Consensus Q H P T (SEQ ID NO:16)	

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FIG 13

>DF-200(VH)\immature-PROT  
 MAVLGLLFCL VTFPSCVLS  
 QVQLEQSGPGGLVQPSQLSITCTVSGFSFTPYGVHWWVQSPGKGLEWLGVIVSGGNTDYNAAFISRLSINKDNSKSQVFFF  
 MNSLQVNNDTAIYYCARNPGRPQNYGMDYWGQGTSVTVSS (SEQ ID NO: 9)

### Anti-KIR heavy variable regions (immature Fabs)

#### Sequences including CDR regions in heavy variable regions

<u>CDR-H1 from clone DF-200</u>	<u>CDR-H2 from clone DF-200</u>
<u>Residues before:</u> Cys-XXX-XXX-XXX <u>Residues after:</u> Trp. Generally Trp-Val or Trp-Ile <u>Length:</u> 10-14 aa <u>Start:</u> Approximately 22-26 aa from the beginning of the secreted protein  <u>GFSFTPYGVH (SEQ ID NO: 10)</u>	<u>Residues before:</u> Leu-Glu-Trp-Ile-Gly but other variations possible <u>Residues after:</u> Lys or Arg / Leu or Ile or Val or Phe or Thr or Ala / Thr or Ser or Ile or Ala <u>Length:</u> 16-20 aa <u>Start:</u> Approximately 15 aa after the end of CDR-H1  <u>VIWSSGGNTDYNAAFIS (SEQ ID NO: 11)</u>
<u>CDR-H3 from clones 4G1, 5D5 and 6C12</u>	
<u>Residues before:</u> Cys-XXX-XXX (Typically Cys-Ala-Arg) <u>Residues after:</u> Trp-Gly-XXX-Gly <u>Length:</u> 3-25 aa <u>Start:</u> Approximately 33 after the end of CDR-H2  <u>NPRPGNYPYGMDY (SEQ ID NO: 12)</u>	

The **secreted, mature VH** starts at:  
 Position 20: residue Q

The VH region ends with residue S and thereafter the constant region (not shown) continues